SEQUENCE LISTING

<110> ZHU, JIAN-KANG
SHI, HUAZHONG
ISHITANI, MANABU
STEVENSON, BECKY

<120> PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS

<130> 205644US20

<140> 09/824,734
<141> 2001-04-04

<150> US 60/194,648
<151> 2000-04-04

<160> 20

<170> PatentIn version 3.1

<210> 1
<211> 6076
<212> DNA
<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(226)

<223>

<220>

<221> CDS

<222> (330)..(380)

<223>

<220>

<221> CDS

<222> (459)..(550)

<223>

<220>

<221> CDS

<222> (631)..(708)

<223>

<220>

<221> CDS

<222> (804)..(961)

<223>

<220>

<221> CDS

<222> (1044)..(1145)

<223>

<220>

<221> CDS

<222> (1235)..(1352)

<223>

<220>

<221> CDS

<222> (1432)..(1484)

<223>

<220>

<221> CDS

<222> (1571)..(1636)

<223>

<220>

<221> CDS

<222> (1738)..(1782)

<223>

<220>

<221> CDS

<222> (1933)..(1985)

<223>

<220>
<221> CDS
<222> (2470)..(2654)
<223>

<220>
<221> CDS
<222> (2767)..(2811)
<223>

<220>
<221> CDS
<222> (2899)..(3006)
<223>

<220>
<221> CDS
<222> (3222)..(3453)
<223>

<220>
<221> CDS
<222> (3531)..(3830)
<223>

<220>

<221> CDS

<222> (4012)..(4109)

<223>

<220>

<221> CDS

<222> (4193)..(4324)

<223>

<220>

<221> CDS

<222> (4407)..(4625)

<223>

<220>

<221> CDS

<222> (4712)..(4915)

<223>

<220>

<221> CDS

<222> (5003)..(5273)

<223>

<220>

<221> CDS

<222> (5375)..(5673)

<223>

<220>

<221> CDS

<222> (5771)..(6073)

<223>

<400> 1

```
atg acg act gta atc gac gcg acg atg gcg tat aga ttt ctg gag gaa        48
Met Thr Thr Val Ile Asp Ala Thr Met Ala Tyr Arg Phe Leu Glu Glu
1               5                  10                  15

gcg acc gat tcg tct tct tct tct tct tct tcc aaa cta gaa tct agc        96
Ala Thr Asp Ser Ser Ser Ser Ser Ser Ser Ser Lys Leu Glu Ser Ser
            20                  25                  30

cct gtc gac gcc gtt ctc ttc gtc gga atg tct ctg gta ctc ggt att       144
Pro Val Asp Ala Val Leu Phe Val Gly Met Ser Leu Val Leu Gly Ile
        35                  40                  45

gct tct agg cac ttg ctt cgt gga act agg gtt cct tac act gtc gct       192
Ala Ser Arg His Leu Leu Arg Gly Thr Arg Val Pro Tyr Thr Val Ala
    50                  55                  60

ctt ctc gtt atc gga att gct ctt gga tct ctc g gttcgatttc              236
Leu Leu Val Ile Gly Ile Ala Leu Gly Ser Leu
65                  70                  75

gttccatgga atttctgatt tcttcatctg ttttaatcct tgaagtcaac gtaatcatgc     296

ttaattgcta attcatgttg tttggtgttt cag aa  tat gga gct aaa cat aac      349
                                  Glu Tyr Gly Ala Lys His Asn
                                                  80

ctt gga aag atc ggc cat gga att cgt atc t gtaagttttt agtttcgaat       400
Leu Gly Lys Ile Gly His Gly Ile Arg Ile
        85                  90

ttttcttctc ttccatggct ggctttgtaa gaactataga atcaatgtta ttgtgcag       458

gg  aat gag atc gat cca gaa ctt ctt tta gct gtt ttt ctt ccg gct       505
```

```
Trp Asn Glu Ile Asp Pro Glu Leu Leu Leu Ala Val Phe Leu Pro Ala
        95                  100                 105

ctt ctt ttc gag agt tcg ttt tca atg gaa gtt cac caa att aag          550
Leu Leu Phe Glu Ser Ser Phe Ser Met Glu Val His Gln Ile Lys
    110                 115                 120

gtttattcct ctggctctaa ttcctagtta agcttaaagg ttaagagaaa taggtactga    610

atacttgcat gattctttag agg tgt ctg gga caa atg gtg tta ctt gct gtc    663
                    Arg Cys Leu Gly Gln Met Val Leu Leu Ala Val
                        125                 130

cct gga gtt ctt att tca aca gct tgt ctt gga tcg ctt gtg aag          708
Pro Gly Val Leu Ile Ser Thr Ala Cys Leu Gly Ser Leu Val Lys
135                 140                 145

gtatgaatta gcctggttgg tattaagtag ctgtcctgaa aacaaagaaa gacaaatcga    768

ttattatgtt atgaaactat acttgctata tgcag gtc acg ttt ccg tat gaa        821
                                        Val Thr Phe Pro Tyr Glu
                                        150                 155

tgg gac tgg aaa acg tcc ttg ttg ctt ggg gga ctt tta agt gct act      869
Trp Asp Trp Lys Thr Ser Leu Leu Leu Gly Gly Leu Leu Ser Ala Thr
                160                 165                 170

gat ccg gtt gct gtt gtt gct ttg cta aag gag ctt ggt gct agt aag      917
Asp Pro Val Ala Val Val Ala Leu Leu Lys Glu Leu Gly Ala Ser Lys
            175                 180                 185

aag cta agc acc ata att gaa ggg gaa tcc ctg atg aat gat gg           961
Lys Leu Ser Thr Ile Ile Glu Gly Glu Ser Leu Met Asn Asp Gly
        190                 195                 200

gtaaatgacg ttatcttctg tcatggtttg gttagttttg acatttatgc tcactcttca   1021

tgatttttaa caacaattcc ag g acg gcg att gtt gtt ttc cag tta ttc       1071
                        Thr Ala Ile Val Val Phe Gln Leu Phe
                            205                 210

tta aag atg gct atg ggg caa aac tct gac tgg agt tct ata atc aaa      1119
Leu Lys Met Ala Met Gly Gln Asn Ser Asp Trp Ser Ser Ile Ile Lys
            215                 220                 225

ttt ctg ctt aaa gtc gca ctt gga gc  gtatgtcttg atctttttc           1165
Phe Leu Leu Lys Val Ala Leu Gly Ala
        230                 235

atctgttgtt agtgatatca agttgctgct gtgttcttat cagtccaacg tgttcttctg   1225

tctatttag t gta ggc att ggt ctg gcg ttt ggc att gca tca gtt att      1274
```

```
                Val Gly Ile Gly Leu Ala Phe Gly Ile Ala Ser Val Ile
                            240                 245

tgg ctc aag ttc ata ttc aat gac act gta ata gag att act ctt aca      1322
Trp Leu Lys Phe Ile Phe Asn Asp Thr Val Ile Glu Ile Thr Leu Thr
250                 255                 260                 265

att gca gtg agc tat ttc gca tac tac act gtacgtcttt ctgtagacct      1372
Ile Ala Val Ser Tyr Phe Ala Tyr Tyr Thr
                270                 275

tgaattcctg tgctaagata ttctctttgt agtaaaactg agagtttatt gtgtgacag   1431

gct caa gag tgg gct ggg gct tct ggt gtt ttg acg gtc atg act ttg      1479
Ala Gln Glu Trp Ala Gly Ala Ser Gly Val Leu Thr Val Met Thr Leu
                280                 285                 290

ggc at  gtaaatttca gtgatctcgt tatttttttt ttccctttct tttgttatca      1534
Gly Met

tttaagaagt ctcttctcat aaaataactg taacag g ttt tat gct gca ttt gca   1589
                                          Phe Tyr Ala Ala Phe Ala
                                              295

agg aca gcc ttt aaa ggt gac agt caa aaa agc ttg cat cac ttc tg      1636
Arg Thr Ala Phe Lys Gly Asp Ser Gln Lys Ser Leu His His Phe Trp
300                 305                 310

gtatttccag aacttgtgga atttggactt gtttttttat attgtaactc tatgtaaaag   1696

gttgatctgt gtgatataaa ttttcccggt aacttgtgca g g gaa atg gtt gca      1750
                                              Glu Met Val Ala

tat att gca aac act ttg ata ttt atc ctc ag  gtaagggtaa attttataga   1802
Tyr Ile Ala Asn Thr Leu Ile Phe Ile Leu Ser
320                 325

ctcatatcat gcttgtgctt gccaacccta aaatagaagc tcatgggtag aaaaaagagc   1862

tattttactg cagtctactc tttagcctgg tgttgcaata ttgactgtgt ttctcgtttt   1922

atgtttgcag t ggt gtt gtc att gct gaa ggc att ctc gac agt gat aag      1972
            Gly Val Val Ile Ala Glu Gly Ile Leu Asp Ser Asp Lys
                            335                 340

att gcc tac caa g gtgccattat ttaatgttga tagtgtacag tatttttttc       2025
Ile Ala Tyr Gln
    345

ctagctaaag taaattttgt gaacatagtt ttgtctgcat tttcgacagt tcactgttaa   2085
```

```
ttgaagatga gatctaagtc attacatagg actcccacct gttatcatag ttttctgtcg   2145

ttgttaacac accttactgt tcatggtctt tggttctcga aggatcacta attccataac   2205

gtgaatcagt tacaagaata agaaaaaaac tggcattatt ggttacgaaa tattgagcga   2265

aagttaccac tgtgctagga ctgagacaat tgtattcttt caccagtctg ttattattat   2325

taagtacctg ttagagatgt actgtcttgg aaccatatat tttttctctg gaaccatatc   2385

tgcataaggc acatgatata cttaacttta actatttttt atattttgga tctaacaact   2445

cttcacgacc caaatttctt acag gg  aat tca tgg cga ttt ctt ttt ctg       2495
                              Gly Asn Ser Trp Arg Phe Leu Phe Leu
                                   350                 355

cta tac gtt tac atc caa cta tcg cgt gtt gtt gtt gtt gga gtt cta      2543
Leu Tyr Val Tyr Ile Gln Leu Ser Arg Val Val Val Val Gly Val Leu
            360                 365                 370

tat cca ctt tta tgt cgt ttt ggc tat ggt ttg gat tgg aaa gaa tcc      2591
Tyr Pro Leu Leu Cys Arg Phe Gly Tyr Gly Leu Asp Trp Lys Glu Ser
        375                 380                 385

att ata ctc gta tgg tct ggt ttg agg ggc gca gtg gct ctt gca ctt      2639
Ile Ile Leu Val Trp Ser Gly Leu Arg Gly Ala Val Ala Leu Ala Leu
    390                 395                 400

tct tta tcc gtg aag gttaatttta agaacatctg ttaaagttgt tcttctctct      2694
Ser Leu Ser Val Lys
405

taaatttctg cacaatgttt ttttccagcc acattgattc tgtgctgact tactcgcact   2754

catttgattc ag caa tca agc gga aat tca cat atc agc aag gag act gga    2805
              Gln Ser Ser Gly Asn Ser His Ile Ser Lys Glu Thr Gly
              410                 415                 420

aca ttg gtaagttagt ctaaagatgt tattgacaac ttaaaatgat tatgcaaatt      2861
Thr Leu

attgttttgt ctcttcatat tctcagttct tttgcag ttt ctt ttc ttc acg ggt    2916
                                         Phe Leu Phe Phe Thr Gly
                                         425                 430

gga att gtg ttc cta act ctg ata gtt aat gga tcc act acc caa ttt     2964
Gly Ile Val Phe Leu Thr Leu Ile Val Asn Gly Ser Thr Thr Gln Phe
                435                 440                 445

gtt cta cgc ctt ctt cgc atg gat att tta cca gcc ccc aag              3006
Val Leu Arg Leu Leu Arg Met Asp Ile Leu Pro Ala Pro Lys
```

```
          450                 455                 460

gtcaaaaact tctctcatac gaataacttt ccgagtttta agtaatcaaa tatatgtgta   3066

aacagagatt tttttgctta tgctttgtat tcatgtgtaa gtgaccgtgt tagcctgagt   3126

ctgagccttt aagctgtata gttcaatagg gtctgtatgt tctagtcagt aatgtattcg   3186

aagaacctta ttagaaacca ctttcctttt gacag aaa cga ata ttg gaa tat       3239
                                        Lys Arg Ile Leu Glu Tyr
                                                            465

aca aag tac gaa atg ttg aat aag gcc tta cga gcg ttt caa gat cta     3287
Thr Lys Tyr Glu Met Leu Asn Lys Ala Leu Arg Ala Phe Gln Asp Leu
            470                 475                 480

gga gac gat gag gag cta gga cct gct gac tgg cct aca gtt gaa agt     3335
Gly Asp Asp Glu Glu Leu Gly Pro Ala Asp Trp Pro Thr Val Glu Ser
        485                 490                 495

tat att tca agc cta aaa ggt tca gaa ggg gaa cta gtt cat cat cct     3383
Tyr Ile Ser Ser Leu Lys Gly Ser Glu Gly Glu Leu Val His His Pro
    500                 505                 510

cac aat ggc tct aaa att gga agt ctt gac cct aaa agt tta aag gac     3431
His Asn Gly Ser Lys Ile Gly Ser Leu Asp Pro Lys Ser Leu Lys Asp
515                 520                 525                 530

ata cgt atg cgg ttc tta aat g gtagttatga tcatgtaccc tccaatatac      3483
Ile Arg Met Arg Phe Leu Asn
                535

tattttacct ggtagattat tgacactttg aaaattggtt gtgtcag gt  gtg caa     3538
                                                Gly Val Gln
                                                        540

gca act tac tgg gag atg ctt gat gag ggc aga ata tct gaa gtt act     3586
Ala Thr Tyr Trp Glu Met Leu Asp Glu Gly Arg Ile Ser Glu Val Thr
                545                 550                 555

gct aat att ttg atg cag tca gtg gat gag gcg ctt gat cag gtt tct     3634
Ala Asn Ile Leu Met Gln Ser Val Asp Glu Ala Leu Asp Gln Val Ser
            560                 565                 570

aca act tta tgt gat tgg aga ggt cta aaa cca cat gtc aat ttc cca     3682
Thr Thr Leu Cys Asp Trp Arg Gly Leu Lys Pro His Val Asn Phe Pro
        575                 580                 585

aat tac tac aac ttt ctt cat tct aaa gtt gtc cca cgc aag ttg gtc     3730
Asn Tyr Tyr Asn Phe Leu His Ser Lys Val Val Pro Arg Lys Leu Val
    590                 595                 600
```

```
aca tac ttt gct gtc gaa aga cta gaa tct gct tgc tac att tct gct    3778
Thr Tyr Phe Ala Val Glu Arg Leu Glu Ser Ala Cys Tyr Ile Ser Ala
605                 610                 615                 620

gcg ttt ctt cgc gca cat aca att gca cga cag caa ttg tat gat ttt    3826
Ala Phe Leu Arg Ala His Thr Ile Ala Arg Gln Gln Leu Tyr Asp Phe
                625                 630                 635

cta g gtatgtacaa tccatactct gcagtctgca tcacactttg aaaacaatga       3880
Leu

ctaagaataa aacttgtacc gtatcatcat taattgtcag agtttttgtt tgcaagtatc   3940

tcaacttagt aagaacaata cattaaccca accctagttt tgtctcatac ttatctatct   4000

tctctacaca g gg  gag agt aat att ggt tcc att gta atc aat gaa agt    4049
            Gly Glu Ser Asn Ile Gly Ser Ile Val Ile Asn Glu Ser
                    640                 645                 650

gaa aag gaa gga gag gaa gca aaa aag ttc ttg gaa aaa gtc cga tct    4097
Glu Lys Glu Gly Glu Glu Ala Lys Lys Phe Leu Glu Lys Val Arg Ser
                655                 660                 665

tca ttt cct cag gttgagagtc ttgtcatttc tttcgggtga cttatctttc       4149
Ser Phe Pro Gln
            670

ttgcggtgag gcacatataa tctttgatta acattggttt cag gtt ctc cgt gtt    4204
                                                Val Leu Arg Val

gtg aaa aca aaa caa gta aca tat tca gtg ttg aat cat tta ctc ggt    4252
Val Lys Thr Lys Gln Val Thr Tyr Ser Val Leu Asn His Leu Leu Gly
675                 680                 685                 690

tac att gaa aac ctc gag aag gtt ggc ttg ttg gag gaa aaa gaa atc    4300
Tyr Ile Glu Asn Leu Glu Lys Val Gly Leu Leu Glu Glu Lys Glu Ile
                695                 700                 705

gct cat ctt cat gat gct gtc cag gtaccaaatt aaagaatctc attccttcaa    4354
Ala His Leu His Asp Ala Val Gln
            710

ctatagtctt gtctcttttg tcttatgctt ttggtcaaat ctatctctgc ag acc ggc   4412
                                                        Thr Gly
                                                        715

ttg aaa aag ctt ttg aga aac cct cca ata gtt aaa ctt cca aaa ttg    4460
Leu Lys Lys Leu Leu Arg Asn Pro Pro Ile Val Lys Leu Pro Lys Leu
            720                 725                 730
```

```
agc gac atg atc acc tca cat ccg tta tcg gtt gct ctt cct cct gca      4508
Ser Asp Met Ile Thr Ser His Pro Leu Ser Val Ala Leu Pro Pro Ala
        735                 740                 745

ttt tgt gaa cct tta aaa cac tcg aaa aaa gaa cca atg aaa ctg cgt      4556
Phe Cys Glu Pro Leu Lys His Ser Lys Lys Glu Pro Met Lys Leu Arg
    750                 755                 760

ggt gtc acg ctt tat aaa gaa ggt tca aag cca act gga gtc tgg ctt      4604
Gly Val Thr Leu Tyr Lys Glu Gly Ser Lys Pro Thr Gly Val Trp Leu
765                 770                 775                 780

att ttt gat ggc atc gtt aag gtaacccaaa acttatcttt tacttttaac         4655
Ile Phe Asp Gly Ile Val Lys
                785

tcgtaagtct gtatgatcta ttaccttcat aactgaatgt tataacaatc ctacag tgg    4714
                                                              Trp

aaa agt aag atc tta agc aac aat cac tcg ctg cat cca act ttt tct      4762
Lys Ser Lys Ile Leu Ser Asn Asn His Ser Leu His Pro Thr Phe Ser
    790                 795                 800

cac ggt agt aca ttg gga ctc tac gaa gtc ctc act ggg aag cca tat      4810
His Gly Ser Thr Leu Gly Leu Tyr Glu Val Leu Thr Gly Lys Pro Tyr
805                 810                 815                 820

ctg tgc gac ttg att aca gat tct atg gtt ctt tgc ttt ttc att gat      4858
Leu Cys Asp Leu Ile Thr Asp Ser Met Val Leu Cys Phe Phe Ile Asp
                825                 830                 835

agc gag aaa att cta tca cta caa tca gat tct acc atc gat gat ttc      4906
Ser Glu Lys Ile Leu Ser Leu Gln Ser Asp Ser Thr Ile Asp Asp Phe
            840                 845                 850

ctt tgg cag gtacgtctct attagaatcc attttagaga gactcatttc              4955
Leu Trp Gln
        855

ttgattgtta agttgcttca actttttttcg gttttttttg tttgcag gaa agt gca     5011
                                                  Glu Ser Ala

ttg gtt ctt ctc aaa ctc ttg cgt cct cag ata ttt gaa agt gtg gca      5059
Leu Val Leu Leu Lys Leu Leu Arg Pro Gln Ile Phe Glu Ser Val Ala
    860                 865                 870

atg caa gaa tta cga gcc ctt gtt tca act gaa agc tcg aaa ctt aca      5107
Met Gln Glu Leu Arg Ala Leu Val Ser Thr Glu Ser Ser Lys Leu Thr
875                 880                 885                 890
```

```
aca tat gtg acg gga gaa tca atc gaa atc gac tgc aac agc att ggt      5155
Thr Tyr Val Thr Gly Glu Ser Ile Glu Ile Asp Cys Asn Ser Ile Gly
                895                 900                 905

tta tta tta gaa gga ttc gta aaa ccg gtt ggt atc aaa gaa gag ctt      5203
Leu Leu Leu Glu Gly Phe Val Lys Pro Val Gly Ile Lys Glu Glu Leu
            910                 915                 920

ata tca tct ccc gcc gca tta tca cct tct aac ggg aat caa agc ttc      5251
Ile Ser Ser Pro Ala Ala Leu Ser Pro Ser Asn Gly Asn Gln Ser Phe
        925                 930                 935

cat aat tca tca gaa gct tca g gtaattaatt gcacagtaca gcaggatcaa       5303
His Asn Ser Ser Glu Ala Ser
    940                 945

acctttttaa atgtcagcga atgatataaa tcgaattaaa tcaaaaatgt gttttgtttt   5363

tttgaccaca g gt  atc atg aga gtc agt ttc tca caa caa gca aca cag     5412
                Gly Ile Met Arg Val Ser Phe Ser Gln Gln Ala Thr Gln
                            950                 955

tat att gtt gag acg aga gca aga gca atc atc ttc aac att gga gca     5460
Tyr Ile Val Glu Thr Arg Ala Arg Ala Ile Ile Phe Asn Ile Gly Ala
    960                 965                 970

ttt gga gct gat agg act cta cat cga aga cca tct tcg tta aca cca     5508
Phe Gly Ala Asp Arg Thr Leu His Arg Arg Pro Ser Ser Leu Thr Pro
975                 980                 985                 990

cca cgt agc tca agc tct gat cag ctt cag  aga tca ttt cgt aaa  gaa   5556
Pro Arg Ser Ser Ser Ser Asp Gln Leu Gln  Arg Ser Phe Arg Lys  Glu
                995                 1000                1005

cac aga ggt ctc  atg agc tgg cct gaa  aat att tac gcc aaa  caa      5601
His Arg Gly Leu  Met Ser Trp Pro Glu  Asn Ile Tyr Ala Lys  Gln
            1010                1015                1020

caa caa gag atc  aat aaa acg aca tta  agt tta tct gaa cga  gca      5646
Gln Gln Glu Ile  Asn Lys Thr Thr Leu  Ser Leu Ser Glu Arg  Ala
        1025                1030                1035

atg caa ctc agc  att ttc ggc agc atg  gtaaaaaaga tctcaatgtt        5693
Met Gln Leu Ser  Ile Phe Gly Ser Met
            1040                1045

gattctttta aaggttgtta tcgatgaact tctcgactaa cctgaaggtt tttatcttct   5753

gatattctcg aatatag gtt aat gtg tac aga  agg agt gta agt ttc  ggt     5803
                Val Asn Val Tyr Arg  Arg Ser Val Ser Phe  Gly
                            1050                1055
```

```
ggg atc tat aat  aac aag tta caa gat  aac ttg ttg tac aaa  aaa      5848
Gly Ile Tyr Asn  Asn Lys Leu Gln Asp  Asn Leu Leu Tyr Lys  Lys
            1060                 1065                 1070

ctt cca cta aac  cca gct caa ggt ctc  gtt tca gcc aaa tca  gaa      5893
Leu Pro Leu Asn  Pro Ala Gln Gly Leu  Val Ser Ala Lys Ser  Glu
            1075                 1080                 1085

agt tca att gtg  acc aag aag cag ctt  gaa acc cgt aaa cat  gcg      5938
Ser Ser Ile Val  Thr Lys Lys Gln Leu  Glu Thr Arg Lys His  Ala
            1090                 1095                 1100

tgt cag ctt cct  ctg aaa ggg gaa agc  agc aca agg caa aat  acg      5983
Cys Gln Leu Pro  Leu Lys Gly Glu Ser  Ser Thr Arg Gln Asn  Thr
            1105                 1110                 1115

atg gtt gaa tca  agc gat gaa gaa gat  gaa gat gaa gga atc  gtt      6028
Met Val Glu Ser  Ser Asp Glu Glu Asp  Glu Asp Glu Gly Ile  Val
            1120                 1125                 1130

gtg aga atc gat  tct ccg agt aaa atc  gtt ttc agg aac gat  cta      6073
Val Arg Ile Asp  Ser Pro Ser Lys Ile  Val Phe Arg Asn Asp  Leu
            1135                 1140                 1145

tga                                                           6076
```

<210> 2

<211> 1146

<212> PRT

<213> Arabidopsis thaliana

<400> 2

```
Met Thr Thr Val Ile Asp Ala Thr Met Ala Tyr Arg Phe Leu Glu Glu
1               5                  10                  15

Ala Thr Asp Ser Ser Ser Ser Ser Ser Ser Ser Lys Leu Glu Ser Ser
            20                  25                  30

Pro Val Asp Ala Val Leu Phe Val Gly Met Ser Leu Val Leu Gly Ile
        35                  40                  45

Ala Ser Arg His Leu Leu Arg Gly Thr Arg Val Pro Tyr Thr Val Ala
```

50 55 60

Leu Leu Val Ile Gly Ile Ala Leu Gly Ser Leu Glu Tyr Gly Ala Lys
65 70 75 80

His Asn Leu Gly Lys Ile Gly His Gly Ile Arg Ile Trp Asn Glu Ile
85 90 95

Asp Pro Glu Leu Leu Leu Ala Val Phe Leu Pro Ala Leu Leu Phe Glu
100 105 110

Ser Ser Phe Ser Met Glu Val His Gln Ile Lys Arg Cys Leu Gly Gln
115 120 125

Met Val Leu Leu Ala Val Pro Gly Val Leu Ile Ser Thr Ala Cys Leu
130 135 140

Gly Ser Leu Val Lys Val Thr Phe Pro Tyr Glu Trp Asp Trp Lys Thr
145 150 155 160

Ser Leu Leu Leu Gly Gly Leu Leu Ser Ala Thr Asp Pro Val Ala Val
165 170 175

Val Ala Leu Leu Lys Glu Leu Gly Ala Ser Lys Lys Leu Ser Thr Ile
180 185 190

Ile Glu Gly Glu Ser Leu Met Asn Asp Gly Thr Ala Ile Val Val Phe
195 200 205

Gln Leu Phe Leu Lys Met Ala Met Gly Gln Asn Ser Asp Trp Ser Ser
210 215 220

Ile Ile Lys Phe Leu Leu Lys Val Ala Leu Gly Ala Val Gly Ile Gly
225 230 235 240

Leu Ala Phe Gly Ile Ala Ser Val Ile Trp Leu Lys Phe Ile Phe Asn
245 250 255

Asp Thr Val Ile Glu Ile Thr Leu Thr Ile Ala Val Ser Tyr Phe Ala

260 265 270

Tyr Tyr Thr Ala Gln Glu Trp Ala Gly Ala Ser Gly Val Leu Thr Val
275 280 285

Met Thr Leu Gly Met Phe Tyr Ala Ala Phe Ala Arg Thr Ala Phe Lys
290 295 300

Gly Asp Ser Gln Lys Ser Leu His His Phe Trp Glu Met Val Ala Tyr
305 310 315 320

Ile Ala Asn Thr Leu Ile Phe Ile Leu Ser Gly Val Val Ile Ala Glu
325 330 335

Gly Ile Leu Asp Ser Asp Lys Ile Ala Tyr Gln Gly Asn Ser Trp Arg
340 345 350

Phe Leu Phe Leu Leu Tyr Val Tyr Ile Gln Leu Ser Arg Val Val Val
355 360 365

Val Gly Val Leu Tyr Pro Leu Leu Cys Arg Phe Gly Tyr Gly Leu Asp
370 375 380

Trp Lys Glu Ser Ile Ile Leu Val Trp Ser Gly Leu Arg Gly Ala Val
385 390 395 400

Ala Leu Ala Leu Ser Leu Ser Val Lys Gln Ser Ser Gly Asn Ser His
405 410 415

Ile Ser Lys Glu Thr Gly Thr Leu Phe Leu Phe Phe Thr Gly Gly Ile
420 425 430

Val Phe Leu Thr Leu Ile Val Asn Gly Ser Thr Thr Gln Phe Val Leu
435 440 445

Arg Leu Leu Arg Met Asp Ile Leu Pro Ala Pro Lys Lys Arg Ile Leu
450 455 460

Glu Tyr Thr Lys Tyr Glu Met Leu Asn Lys Ala Leu Arg Ala Phe Gln

465 470 475 480

Asp Leu Gly Asp Asp Glu Glu Leu Gly Pro Ala Asp Trp Pro Thr Val
485 490 495

Glu Ser Tyr Ile Ser Ser Leu Lys Gly Ser Glu Gly Glu Leu Val His
500 505 510

His Pro His Asn Gly Ser Lys Ile Gly Ser Leu Asp Pro Lys Ser Leu
515 520 525

Lys Asp Ile Arg Met Arg Phe Leu Asn Gly Val Gln Ala Thr Tyr Trp
530 535 540

Glu Met Leu Asp Glu Gly Arg Ile Ser Glu Val Thr Ala Asn Ile Leu
545 550 555 560

Met Gln Ser Val Asp Glu Ala Leu Asp Gln Val Ser Thr Thr Leu Cys
565 570 575

Asp Trp Arg Gly Leu Lys Pro His Val Asn Phe Pro Asn Tyr Tyr Asn
580 585 590

Phe Leu His Ser Lys Val Val Pro Arg Lys Leu Val Thr Tyr Phe Ala
595 600 605

Val Glu Arg Leu Glu Ser Ala Cys Tyr Ile Ser Ala Ala Phe Leu Arg
610 615 620

Ala His Thr Ile Ala Arg Gln Gln Leu Tyr Asp Phe Leu Gly Glu Ser
625 630 635 640

Asn Ile Gly Ser Ile Val Ile Asn Glu Ser Glu Lys Glu Gly Glu Glu
645 650 655

Ala Lys Lys Phe Leu Glu Lys Val Arg Ser Ser Phe Pro Gln Val Leu
660 665 670

Arg Val Val Lys Thr Lys Gln Val Thr Tyr Ser Val Leu Asn His Leu

675 680 685

Leu Gly Tyr Ile Glu Asn Leu Glu Lys Val Gly Leu Leu Glu Glu Lys
690 695 700

Glu Ile Ala His Leu His Asp Ala Val Gln Thr Gly Leu Lys Lys Leu
705 710 715 720

Leu Arg Asn Pro Pro Ile Val Lys Leu Pro Lys Leu Ser Asp Met Ile
725 730 735

Thr Ser His Pro Leu Ser Val Ala Leu Pro Pro Ala Phe Cys Glu Pro
740 745 750

Leu Lys His Ser Lys Lys Glu Pro Met Lys Leu Arg Gly Val Thr Leu
755 760 765

Tyr Lys Glu Gly Ser Lys Pro Thr Gly Val Trp Leu Ile Phe Asp Gly
770 775 780

Ile Val Lys Trp Lys Ser Lys Ile Leu Ser Asn Asn His Ser Leu His
785 790 795 800

Pro Thr Phe Ser His Gly Ser Thr Leu Gly Leu Tyr Glu Val Leu Thr
805 810 815

Gly Lys Pro Tyr Leu Cys Asp Leu Ile Thr Asp Ser Met Val Leu Cys
820 825 830

Phe Phe Ile Asp Ser Glu Lys Ile Leu Ser Leu Gln Ser Asp Ser Thr
835 840 845

Ile Asp Asp Phe Leu Trp Gln Glu Ser Ala Leu Val Leu Leu Lys Leu
850 855 860

Leu Arg Pro Gln Ile Phe Glu Ser Val Ala Met Gln Glu Leu Arg Ala
865 870 875 880

Leu Val Ser Thr Glu Ser Ser Lys Leu Thr Thr Tyr Val Thr Gly Glu

885 890 895

Ser Ile Glu Ile Asp Cys Asn Ser Ile Gly Leu Leu Leu Glu Gly Phe
900 905 910

Val Lys Pro Val Gly Ile Lys Glu Glu Leu Ile Ser Ser Pro Ala Ala
915 920 925

Leu Ser Pro Ser Asn Gly Asn Gln Ser Phe His Asn Ser Ser Glu Ala
930 935 940

Ser Gly Ile Met Arg Val Ser Phe Ser Gln Gln Ala Thr Gln Tyr Ile
945 950 955 960

Val Glu Thr Arg Ala Arg Ala Ile Ile Phe Asn Ile Gly Ala Phe Gly
965 970 975

Ala Asp Arg Thr Leu His Arg Arg Pro Ser Ser Leu Thr Pro Pro Arg
980 985 990

Ser Ser Ser Ser Asp Gln Leu Gln Arg Ser Phe Arg Lys Glu His Arg
995 1000 1005

Gly Leu Met Ser Trp Pro Glu Asn Ile Tyr Ala Lys Gln Gln Gln
1010 1015 1020

Glu Ile Asn Lys Thr Thr Leu Ser Leu Ser Glu Arg Ala Met Gln
1025 1030 1035

Leu Ser Ile Phe Gly Ser Met Val Asn Val Tyr Arg Arg Ser Val
1040 1045 1050

Ser Phe Gly Gly Ile Tyr Asn Asn Lys Leu Gln Asp Asn Leu Leu
1055 1060 1065

Tyr Lys Lys Leu Pro Leu Asn Pro Ala Gln Gly Leu Val Ser Ala
1070 1075 1080

Lys Ser Glu Ser Ser Ile Val Thr Lys Lys Gln Leu Glu Thr Arg

1085 1090 1095

Lys His Ala Cys Gln Leu Pro Leu Lys Gly Glu Ser Ser Thr Arg
1100 1105 1110

Gln Asn Thr Met Val Glu Ser Ser Asp Glu Glu Asp Glu Asp Glu
1115 1120 1125

Gly Ile Val Val Arg Ile Asp Ser Pro Ser Lys Ile Val Phe Arg
1130 1135 1140

Asn Asp Leu
1145

<210> 3

<211> 822

<212> PRT

<213> Cricetulus griseus

<400> 3

Met Met Leu Arg Trp Ser Gly Ile Trp Gly Leu Ser Pro Pro Arg Ile
1 5 10 15

Phe Pro Ser Leu Leu Val Val Val Ala Leu Val Gly Leu Leu Pro Val
20 25 30

Leu Arg Ser His Gly Leu Gln Pro Ser Pro Thr Ala Asn Thr Ile Arg
35 40 45

Gly Ala Glu Pro Pro Arg Glu Arg Ser Ile Gly Asp Val Thr Thr Ala
50 55 60

Pro Ser Glu Pro Val His His Pro Asp Asp Arg Asn Leu Thr Asn Leu
65 70 75 80

His Ile Glu His Gly Ala Lys Thr Leu Arg Lys Ala Phe Pro Val Leu

85 90 95

Asp Ile Asp Tyr Leu His Val Arg Thr Pro Phe Glu Ile Ser Leu Trp
100 105 110

Ile Leu Leu Ala Cys Leu Met Lys Ile Gly Phe His Val Ile Pro Thr
115 120 125

Ile Ser Ser Ile Val Pro Glu Ser Cys Leu Leu Ile Val Val Gly Leu
130 135 140

Leu Val Gly Gly Leu Ile Lys Gly Val Gly Glu Thr Pro Pro Phe Leu
145 150 155 160

Gln Ser Asp Val Phe Phe Leu Phe Leu Leu Pro Pro Ile Ile Leu Asp
165 170 175

Ala Gly Tyr Phe Leu Pro Leu Arg Gln Phe Thr Glu Asn Leu Gly Thr
180 185 190

Ile Leu Ile Phe Ala Val Val Gly Thr Leu Trp Asn Ala Phe Phe Leu
195 200 205

Gly Gly Leu Leu Tyr Ala Val Cys Leu Val Gly Gly Glu Gln Ile Asn
210 215 220

Asn Ile Gly Leu Leu Asp Thr Leu Leu Phe Gly Ser Ile Ile Ser Ala
225 230 235 240

Val Asp Pro Val Ala Val Val Ala Val Phe Glu Glu Ile His Ile Asn
245 250 255

Glu Leu Leu His Ile Leu Val Phe Gly Glu Ser Leu Leu Asn Asp Ala
260 265 270

Val Thr Val Val Leu Tyr His Leu Phe Glu Glu Phe Ala Asn Tyr Asp
275 280 285

Ser Ile Gly Ile Ser Asp Ile Phe Leu Gly Phe Leu Ser Phe Phe Val

290 295 300

Val Ala Leu Gly Gly Val Phe Val Gly Val Val Tyr Gly Val Ile Ala
305 310 315 320

Ala Phe Thr Ser Arg Phe Thr Ser His Ile Arg Val Ile Glu Pro Leu
325 330 335

Phe Val Phe Leu Tyr Ser Tyr Met Ala Tyr Leu Ser Ala Glu Leu Phe
340 345 350

His Leu Ser Gly Ile Met Ala Leu Ile Ala Ser Gly Val Val Met Arg
355 360 365

Pro Tyr Val Glu Ala Asn Ile Ser His Lys Ser His Thr Thr Ile Lys
370 375 380

Tyr Phe Leu Lys Met Trp Ser Ser Val Ser Glu Thr Leu Ile Phe Ile
385 390 395 400

Phe Leu Gly Val Ser Thr Val Ala Gly Ser His Gln Trp Asn Trp Thr
405 410 415

Phe Val Ile Ser Thr Leu Leu Phe Cys Leu Ile Ala Arg Val Leu Gly
420 425 430

Val Leu Val Leu Thr Trp Phe Ile Asn Lys Phe Arg Ile Val Lys Leu
435 440 445

Thr Pro Lys Asp Gln Phe Ile Ile Ala Tyr Gly Gly Leu Arg Gly Ala
450 455 460

Ile Ala Phe Ser Leu Gly Tyr Leu Met Asp Lys Lys His Phe Pro Met
465 470 475 480

Cys Asp Leu Phe Leu Thr Ala Ile Ile Thr Val Ile Phe Phe Thr Val
485 490 495

Phe Val Gln Gly Met Thr Ile Arg Pro Leu Val Asp Leu Leu Ala Val

500 505 510

Lys Lys Lys Gln Glu Thr Lys Arg Ser Ile Asn Glu Glu Ile His Thr
515 520 525

Gln Phe Leu Asp His Leu Leu Thr Gly Ile Glu Asp Ile Cys Gly His
530 535 540

Tyr Gly His His His Trp Lys Asp Lys Leu Asn Arg Phe Asn Lys Lys
545 550 555 560

Tyr Val Lys Lys Cys Leu Ile Ala Gly Glu Arg Ser Lys Glu Pro Gln
565 570 575

Leu Ile Ala Phe Tyr His Lys Met Glu Met Lys Gln Ala Ile Glu Leu
580 585 590

Val Glu Ser Gly Gly Met Gly Lys Ile Pro Ser Ala Val Ser Thr Val
595 600 605

Ser Met Gln Asn Ile His Pro Lys Ser Met Ala Ser Glu Arg Ile Leu
610 615 620

Pro Ala Leu Ser Lys Asp Lys Glu Glu Glu Ile Arg Lys Ile Leu Arg
625 630 635 640

Ser Asn Leu Gln Lys Thr Arg Gln Arg Leu Arg Ser Tyr Asn Arg His
645 650 655

Thr Leu Val Ala Asp Pro Tyr Glu Glu Ala Trp Asn Gln Met Leu Leu
660 665 670

Arg Arg Gln Lys Ala Arg Gln Leu Glu Gln Lys Met Ser Asn Tyr Leu
675 680 685

Thr Val Pro Ala His Lys Leu Asp Ser Pro Thr Met Ser Arg Ala Arg
690 695 700

Ile Gly Ser Asp Pro Leu Ala Tyr Glu Pro Lys Ala Asp Leu Pro Val

705 710 715 720

Ile Thr Ile Asp Pro Ala Ser Pro Gln Ser Pro Glu Ser Val Asp Leu
725 730 735

Val Asn Glu Glu Leu Lys Ala Lys Val Leu Gly Val Asn Arg Asp Pro
740 745 750

Thr Arg Leu Thr Arg Gly Glu Glu Asp Glu Asp Glu Asp Glu Asp Gly
755 760 765

Val Ile Met Met Arg Arg Lys Glu Pro Ser Ser Pro Gly Thr Asp Val
770 775 780

Phe Thr Pro Ala Pro Met Tyr Ser Pro Ser Ser Gln Arg Ile Gln Arg
785 790 795 800

Cys Leu Ser Asp Pro Gly Pro His Pro Glu Pro Gly Glu Gly Glu Pro
805 810 815

Phe Ile Pro Lys Gly Glu
820

<210> 4

<211> 424

<212> PRT

<213> Pseudomonas aeruginosa

<400> 4

Met Leu Asp Leu Val Ala Ala Phe Ile Ala Leu Thr Thr Leu Leu Thr
1 5 10 15

Tyr Val Asn Tyr Arg Phe Ile Arg Leu Pro Pro Thr Ile Gly Val Met
20 25 30

Ala Thr Ala Leu Val Phe Ser Leu Ile Val Gln Gly Leu Ser Glu Leu

35 40 45

Gly Tyr Pro Ile Leu Glu Val Glu Met Gln Glu Ile Ile Arg Arg Ile
50 55 60

Asp Phe Ser Glu Val Leu Met Thr Trp Phe Leu Pro Ala Leu Leu Phe
65 70 75 80

Ala Gly Ala Leu His Val Asp Leu Ser Asp Leu Arg Ser Tyr Lys Trp
85 90 95

Pro Ile Gly Leu Leu Ala Thr Ala Gly Val Leu Ile Ala Thr Phe Val
100 105 110

Ile Gly Gly Leu Ala Tyr Tyr Thr Phe Pro Leu Phe Gly Trp Gln Val
115 120 125

Asp Phe Ile Tyr Cys Leu Leu Phe Gly Ala Leu Ile Ser Pro Thr Asp
130 135 140

Pro Ile Ala Val Leu Gly Ile Leu Lys Ser Ala Gly Ala Pro Lys Pro
145 150 155 160

Leu Ala Thr Thr Ile Val Gly Glu Ser Leu Phe Asn Asp Gly Thr Ala
165 170 175

Val Val Val Phe Ala Ile Ile Leu Gly Ile Leu Gln Leu Gly Glu Ala
180 185 190

Pro Thr Val Ser Ala Thr Ala Ile Leu Phe Val Gln Glu Ala Ile Gly
195 200 205

Gly Val Val Phe Gly Ala Val Leu Gly Tyr Gly Val Phe Val Met Met
210 215 220

Arg Gly Ile Asp Gln Tyr Gln Val Glu Val Met Leu Thr Leu Ala Leu
225 230 235 240

Val Ile Gly Gly Ala Ala Leu Ala Ala Arg Leu His Val Ser Ala Pro

245 250 255

Ile Ala Met Val Val Ala Gly Leu Ile Ile Gly Asn His Gly Arg His
260 265 270

Tyr Ala Met Ser Asp Glu Thr Arg Arg Tyr Val Asp Lys Phe Trp Glu
275 280 285

Leu Ile Asp Glu Ile Leu Asn Ala Leu Leu Phe Ala Leu Ile Gly Leu
290 295 300

Glu Leu Leu Leu Leu Pro Phe Ser Trp Leu His Val Ala Ala Ala Phe
305 310 315 320

Ala Leu Gly Gly Ala Val Leu Val Ser Arg Leu Leu Thr Val Gly Pro
325 330 335

Ala Ile Leu Val Leu Arg Arg Phe Arg Gly Ala Asn Arg Gln Val Pro
340 345 350

Ala Gly Thr Ile Arg Ile Leu Val Trp Gly Gly Leu Arg Gly Gly Val
355 360 365

Ser Val Ala Leu Ala Leu Ser Leu Pro Leu Gly Pro Glu Arg Asp Leu
370 375 380

Ile Leu Ser Leu Thr Tyr Ile Val Val Leu Val Ser Ile Leu Leu Gln
385 390 395 400

Gly Leu Ser Ile Gly Pro Leu Val Arg Arg Ile Tyr Ala Gly Gln Pro
405 410 415

Leu Glu Lys Ser Glu Gly Ala His
420

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 5
ggatgatgat cgattcggat 20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 6
atctgactca taggatatcg 20

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 7
ccttcacatc caaaacccac 20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 8
gcacataccc acaaccagaa 20

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 9
gaatgttttg aaggatatct cag 23

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 10
gaaaaatgga gcacgaaatg c 21

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 11
cccgagatta atacacaatc 20

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 12
gcagattatg taattgtgac c 21

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 13
tcgtgtttac cgggtcggat 20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 14
tgatgagaat cttagcgagc 20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 15
tggtaagacc aaattacact c 21

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 16
cgtaattaaa atgtgttaaa ccg 23

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 17
aaccgcatag tacaatgcag 20

<210> 18

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 18
cggtaaagat caactaataa cg 22

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 19

aacggaaacg gcaactagac 20

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 20
accctaaatg tttcgattcg 20